

SEQUENCE LISTING

SEQ ID NO: 1

Sequence Length: 40

Sequence Type: Nucleic acid

Strand dn ss: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

ACTAGTCGAC ATGAAGTTGC CTGTTAGGCT GTTGGTGCTG

40

SEQ ID NO: 2

Sequence Length: 39

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

ACTAGTCGAC ATGGAGWCAG ACACACTCCT GYTATGGGT

39

SEQ ID NO: 3

Sequence Length: 40

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

ACTAGTCGAC ATGAGTGTGC TCACTCAGGT CCTGGSGTTG

40

SEQ ID NO: 4

Sequence Length: 43

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

ACTAGTCGAC ATGAGGRCCC CTGCTCAGWT TYTTGGMWTC TTG

43

SEQ ID NO: 5

Sequence Length: 40

DRAFT DRAFT DRAFT

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

ACTAGTCGAC ATGGATTWC AGGTGCAGAT TWTCAAGCTTC

40

SEQ ID NO: 6

Sequence Length: 37

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

ACTAGTCGAC ATGAGGCKCY YTGYTSAGYT YCTGRGG

37

SEQ ID NO: 7

Sequence Length: 41

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

ACTAGTCGAC ATGGGCWTCA AGATGGAGTC ACAKWYYCWG G

41

SEQ ID NO: 8

Sequence Length: 41

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

ACTAGTCGAC ATGTGGGAY CTKTTTYCMM TTTTTCAATT G

41

SEQ ID NO: 9

Sequence Length: 35

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

DRAFTED BY [REDACTED]

Molecular Typ : Synth tic DNA

Sequence

ACTAGTCGAC ATGGGTRTCCW CASCTCAGTT CCTTG

35

SEQ ID NO: 10

Sequence Length: 37

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

ACTAGTCGAC ATGTATATAT GTTTGTTGTC TATTCT

37

SEQ ID NO: 11

Sequence Length: 38

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

ACTAGTCGAC ATGGAAGCCC CAGCTCAGCT TCTCTTCC

38

SEQ ID NO: 12

Sequence Length: 27

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

GGATCCCGGG TGGATGGTGG GAAGATG

27

SEQ ID NO: 13

Sequence Length: 37

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

ACTAGTCGAC ATGAAATGCA GCTGGGTCA STTCTTC

37

DRAFT EDITION 12/2000

SEQ ID NO: 14
Sequence Length: 36
Sequence Type: Nucleic acid
Strandedness: Singl
Topology: Linear
Molecular Type: Synthetic DNA
Sequence

ACTAGTCGAC ATGGGATGGA GCTRTATCAT SYTCTT

36

SEQ ID NO: 15
Sequence Length: 37
Sequence Type: Nucleic acid
Strandedness: Single
Topology: Linear
Molecular Type: Synthetic DNA
Sequence

ACTAGTCGAC ATGAAGWTGT GCTTAAACTG GGTTTTT

37

SEQ ID NO: 16
Sequence Length: 35
Sequence Type: Nucleic acid
Strandedness: Single
Topology: Linear
Molecular Type: Synthetic DNA
Sequence

ACTAGTCGAC ATGRACCTTG GGYTCAGCTT GRTTT

35

SEQ ID NO: 17
Sequence Length: 40
Sequence Type: Nucleic acid
Strandedness: Single
Topology: Linear
Molecular Type: Synthetic DNA
Sequence

ACTAGTCGAC ATGGACTCCA GGCTCAATT AGTTTCCCTT

40

SEQ ID NO: 18
Sequence Length: 37
Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

ACTAGTCGAC ATGGCTGTCY TRGSGCTRCT CTTCTGC

37

SEQ ID NO: 19

Sequence Length: 36

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

ACTAGTCGAC ATGGRATGGA GCKGGRTCTT TMTCTT

36

SEQ ID NO: 20

Sequence Length: 33

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

ACTAGTCGAC ATGAGAGTGC TGATTCTTT GTG

33

SEQ ID NO: 21

Sequence Length: 40

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

ACTAGTCGAC ATGGMTTGGG TGTGGAMCTT GCTATTCCCTG

40

SEQ ID NO: 22

Sequence Length: 37

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequ nc

ACTAGTCGAC ATGGGCAGAC TTACATTCTC ATTCCCTG

37

SEQ ID NO: 23

S quence Length: 38

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

ACTAGTCGAC ATGGATTTTG GGCTGATTGT TTTTATTG

38

SEQ ID NO: 24

Sequence Length: 37

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

ACTAGTCGAC ATGATGGTGT TAAGTCTTCT GTACCTG

37

SEQ ID NO: 25

Sequence Length: 28

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

GGATCCCCGG CCAGTGGATA GACAGATG

28

SEQ ID NO: 26

Sequence Length: 382

Sequence Type: Nucleic acid

Strandedness: Double

Topology: Linear

Molecular Type: cDNA

Original Source

Organism: Mouse

Immediate Source

Clone: pUC-M21-V₁
Features: 1..72 sig peptide
73..382 mat peptide

Sequence

ATG GAG TCA CAT ATT CAG GTC TTT GTA TAC ATG TTG CTG TGG TTG TCT	48
Met Glu Ser His Ile Gln Val Phe Val Tyr Met Leu Leu Trp Leu Ser	
5 10 15	
GGT GTT GAT GGA GAC ATT GTG ATG ACC CAG TCT CAA AAA TTC ATG TCC	96
Gly Val Asp Gly Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser	
20 25 30	
ACA TCA GTA GGA GAC AGG GTC AGC GTC ACC TGC AAG GCC AGT CAG AAT	144
Thr Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn	
35 40 45	
GTG GGT ACT AAT GTA GCC TGG TAT CAA CAG AAA CCA GGG CAA TCT CCT	192
Val Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro	
50 55 60	
AAA CCA CTG ATT TAC TCG GCA TCC TAT CGG TAC AGT GGA GTC CCT GAT	240
Lys Pro Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Asp	
65 70 75 80	
CGC TTC ACA GGC AGT GGA TCT GGG ACA GAT TTC ACT CTC ACC ATC ACC	288
Arg Phe Thr Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr	
85 90 95	
AAT GTG CAG TCT GAA GAC TTG GCA GAC TAT TTC TGT CAG CAA TAT AAC	336
Asn Val Gln Ser Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln Tyr Asn	
100 105 110	
AGC TAT CCT CGG GCG TTC CGT CGA GGC ACC AAA CTG GAA ATC AAA C	382
Ser Tyr Pro Arg Ala Phe Gly Gly Thr Lys Leu Glu Ile Lys	
115 120 125	

SEQ ID NO: 27

Sequence Length: 409

Sequence Type: Nucleic acid

Strandedness: Double

Topology: Linear

Molecular Type: cDNA

Original Source

Organism: Mouse

Immediate Source

Clone: pUC-M21-V_{II}

Features: 1..57 sig peptide

58..409 mat peptide

Sequence

ATG AAA TGC AGC TGG GTC ATG TTC TTC CTG ATG GCA GTG GTT ACA GGG 48
Met Lys Cys Ser Trp Val Met Phe Phe Leu Met Ala Val Val Thr Gly
5 10 15

GTC AAT TCA GAG GTT CAG CTG CAG CAG TCT GGG GCA GAG CTT GTG AAG 96
Val Asn Ser Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys
20 25 30

CCA GGG GCC TCA GTC AAG TTG TCC TGC ACA GCT TCT GGC TTC AAC ATT 144
Pro Gly Ala Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile
35 40 45

AAA GAC ACC TAT ATA CAC TGG GCG AAG CAG AGG CCT GAA CAG GGC CTG 192
Lys Asp Thr Tyr Ile His Trp Ala Lys Gln Arg Pro Glu Gln Gly Leu
50 55 60

GAG TGG ATT GGA AGG ATT GAT CCT GCG GAT GGT AAT ACT AAA TAT GAC 240
Glu Trp Ile Gly Arg Ile Asp Pro Ala Asp Gly Asn Thr Lys Tyr Asp
65 70 75 80

CCG AAG TTC CAG GGC AAG GCC ACT ATA ACA GCA GAC ACA TCC TCC AAC 288
Pro Lys Phe Gln Gly Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn
85 90 95

ACA GCC TAC CTG CAG CTC AGC AGC CTG ACA TCT GAG GAC ACT GCC GTC 336
Thr Ala Tyr Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val
100 105 110

TAT TAC TGT GCT TCG GCG TAC TAT GTT AAC CAG GAC TAC TGG GGT CAA 384
Tyr Tyr Cys Ala Ser Ala Tyr Tyr Val Asn Gln Asp Tyr Trp Gly Gln
115 120 125

GGA ACC TCA GTC ACC GTC TCC TCA G 409
Gly Thr Ser Val Thr Val Ser Ser
130 135

SEQ ID NO: 28
Sequence Length: 34
Sequence Type: Nucleic acid
Strandedness: Single
Topology: Linear
Molecular Type: Synthetic DNA
Sequence
GATAAGCTTC CACCATGGGC TTCAAGATGG AGTC 34
SEQ ID NO: 29
Sequence Length: 34
Sequence Type: Nucleic acid
Strandedness: Single
Topology: Linear
Molecular Type: Synthetic DNA
Sequence
GGCGGATCCA CTCACGTTTG ATTTCCAGTT TGGT 34
SEQ ID NO: 30
Sequence Length: 43
Sequence Type: Nucleic acid
Strandedness: Single
Topology: Linear
Molecular Type: Synthetic DNA
Sequence
GATAAGCTTC CACCATGAAA TGCAGCTGGG TCATGTTCTT CCT 43
SEQ ID NO: 31
Sequence Length: 34
Sequence Type: Nucleic acid
Strandedness: Single
Topology: Linear
Molecular Type: Synthetic DNA
Sequence
GGCGGATCCA CTCACCTGAG GAGACGGTGA CTGA 34

SEQ ID NO: 32
Sequence Length: 18
Sequence Type: Nucleic acid
Strandedness: Single
Topology: Linear
Molecular Type: Synthetic DNA
Sequence

CAGACAGTGG TTCAAAGT

18

SEQ ID NO: 33

Sequence Length: 26
Sequence Type: Nucleic acid
Strandedness: Single
Topology: Linear
Molecular Type: Synthetic DNA
Sequence

GAATTCGGAT CCACTCACGT TTGATT

26

SEQ ID NO: 34

Sequence Length: 44
Sequence Type: Nucleic acid
Strandedness: Single
Topology: Linear
Molecular Type: Synthetic DNA
Sequence

AGTCAGAATG TGGGTACTAA TGTAGCCTGG TACCAGCAGA AGCC

44

SEQ ID NO: 35

Sequence Length: 38
Sequence Type: Nucleic acid
Strandedness: Single
Topology: Linear
Molecular Type: Synthetic DNA
Sequence

TCCTATCGGT ACAGTGTTGT GCCAAGCAGA TTCAGCGG

38

SEQ ID NO: 36

Sequence Length: 47

Sequence Type: Nucleic acid

Strandedn ss: Singl

Topology: Linear

Molecular Typ : Synthetic DNA

Sequence

GCTACCTACT ACTGCCAGCA ATATAACAGC TATCCTCGGG CGTTCGG

47

SEQ ID NO: 37

Sequence Length: 44

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

ACATTAGTAC CCACATTCTG ACTGGCCTTA CAGGTGATGG TCAC

44

SEQ ID NO: 38

Sequence Length: 47

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

GGCACACCCAC TGTACCGATA GGATGCCGAG TAGATCAGCA GCTTG

47

SEQ ID NO: 39

Sequence Length: 44

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

GGATAGCTGT TATATTGCTG GCAGTAGTAG GTAGCGATGT CCTC

44

SEQ ID NO: 40

Sequence Length: 379

Sequence Type: Nucleic acid

Strandedness: Double

Topology: Linear

Molecular Type: Synthetic

Original Source

Organism: Mouse and human

Immediat Source

Clon : HEF-RVL-M21a-gk

Amino acid -19--1:leader

Amino acid 1 - 23:FR1

Amino acid 24 - 34:CDR1

Amino acid 35 - 49:FR2

Amino acid 50 - 56:CDR2

Amino acid 57 - 88:FR3

Amino acid 89 - 97:CDR3

Amino acid 98 - 107:FR4

Sequence

ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT	48
Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly	
-19 15 -10 -5	
GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA ACC AGC CTG AGC GCC	96
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala	
-1 1 5 10	
AGC GTG GGT GAC AGA GTG ACC ATC ACC TGT AAG GCC AGT CAG AAT GTG	144
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val	
15 20 25	
GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA AAG GCT CCA AAG	192
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys	
30 35 40	
CTG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA	240
Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg	
45 50 55 60	
TTC AGC GGT AGC GGT AGC GGT ACC GAC TTC ACC ATC AGC AGC	288
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser	
65 70 75	

CTC CAG CCA GAG GAC ATC GCC ACC TAC TAC TGC CAG CAA TAT AAC AGC
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser
80 85 90

336

TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA C
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
95 100 105

379

SEQ ID NO: 41

Sequence Length: 31

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

GGTACCGACT ACACCTTCAC CATCAGCAGC C

31

SEQ ID NO: 42

Sequence Length: 31

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

GGTGAAGGTG TAGTCGGTAC CGCTACCGCT A

31

SEQ ID NO: 43

Sequence Length: 379

Sequence Type: Nucleic acid

Strandedness: Double

Topology: Linear

Molecular Type: Synthetic

Original Source

Organism: Mouse and human

Immediate Source

Clone: HEF-RVL-M21b-gk

Amino acid -19--1:leader

Amino acid 1 - 23:FR1

Amino acid 24 - 34:CDR1

Amino acid 35 - 49:FR2
Amino acid 50 - 56:CDR2
Amino acid 57 - 88:FR3
Amino acid 89 - 97:CDR3
Amino acid 98 - 107:FR4

Sequence

ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA CCT ACA GGT 48
Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly
-19 -15 -10 -5

GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC 96
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala
-1 1 5 10

ACC GTG GGT GAC AGA GTG ACC ATC ACC TGT AAG GCC AGT CAG AAT GTG 144
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val
15 20 25

GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA AAG GCT CCA AAG 192
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
30 35 40

CTG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA 240
Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg
45 50 55 60

TTC AGC GGT AGC GGT ACT GGT ACC GAC TAC ACC TTC ACC ATC AGC AGC 288
Phe Ser Gly Ser Gly Thr Asp Tyr Thr Phe Thr Ile Ser Ser
65 70 75

CTC CAG CCA GAG GAC ATC GCC ACC TAC TAC TGC CAG CAA TAT AAC AGC 336
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser
80 85 90

TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA C 379
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
95 100 105

SEQ ID NO: 44

Sequence Length: 29

Sequence Type: Nucleic acid

Strandedness: Singl
Topology: Linear
Mol cular Type: Synth tic DNA
Sequence

GCTACCTACT TCTGCCAGCA ATATAAACAG

29

SEQ ID NO: 45

Sequence Length: 29

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

TGCTGGCAGA AGTAGGTAGC GATGTCCTC

29

SEQ ID NO: 46

Sequence Length: 379

Sequence Type: Nucleic acid

Strandedness: Double

Topology: Linear

Molecular Type: Synthetic

Original Source

Organism: Mouse and human

Immediate Source

Clone: HEF-RVL-M21c-gx

Amino acid -19--1:leader

Amino acid 1 - 23:FR1

Amino acid 24 - 34:CDR1

Amino acid 35 - 49:FR2

Amino acid 50 - 56:CDR2

Amino acid 57 - 88:FR3

Amino acid 89 - 97:CDR3

Amino acid 98 - 107:FR4

Sequence

ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT

Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly

-19

-15

-10

-5

48

GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC
 Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala
 -1 1 5 10

AGC GTG GGT GAC AGA GTG ACC ATC ACC TGT AAG CCC AGT CAG AAT GTG 144
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val
15 20 25

GGT ACT AAT GTA GGC TCG TAC CAG CAG AAG CCA GGA AAG GCT CCA AAG 192
Gly Thr Asn Val Ala Ile Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
30 35 40

CTG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA 240
 Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg
 45 50 55 60

TTC AGC GGT AGC GGT ACC GAC TTC ACC TTC ACC ATC AGC AGC
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser
63 70 75

CTC CAG CCA GAG GAC ATC GCC ACC TAC TTC TGC CAG CAA TAT AAC AGC
 Leu Gln Pro Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Tyr Asn Ser
 80 85 90

TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA C 379
 Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 95 100 105

SEO ID NO: 47

Sequence Length: 379

Sequence Type: Nucleic acid

Strandedness: Double

Topology: Linear

Molecular Type: Synthetic

Original Source

Organism: Mouse and human

Immediate Source

Clone: HEF-RVL-M21d-qk

Amino acid -19--1:leader

Amino acid 1 = 23:FR1

Amino acid 24 - 34:CDR1
Amino acid 35 - 49:FR2
Amino acid 50 - 56:CDR2
Amino acid 57 - 88:FR3
Amino acid 89 - 97:CDR3
Amino acid 98 - 107:FR4

Sequence

ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT 48
Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly
-19 -15 -10 -3

GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC 96
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala
-1 1 5 10

AGC GTG GGT GAC AGA GTG ACC ATC ACC TGT AAG GCC AGT CAG AAT GTG 144
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val
15 20 25

GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA AAG CCT CCA AAG 192
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
30 35 40

CTG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA 240
Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg
45 50 55 60

TTC AGC GGT AGC GGT AGC GGT ACC GAC TAC AGC TTC ACC ATC AGC AGC 288
Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Phe Thr Ile Ser Ser
65 70 75

CTC CAG CCA GAG GAC ATC GCC ACC TAC TTC TGC CAG CAA TAT AAC AGC 336
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Tyr Asn Ser
80 85 90

TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA C 379
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
95 100 105

SEQ ID NO: 48

Sequence Length: 29

~~S quenc~~ Type: Nucleic acid

~~Strandedness:~~ Single

~~Topology:~~ Linear

~~Molecular Type:~~ Synthetic DNA

~~Sequence~~

TGACAGAGTG TCCGTACCT GTAAGGCCA

29

SEQ ID NO: 49

Sequence Length: 29

~~Sequence Type:~~ Nucleic acid

~~Strandedness:~~ Single

~~Topology:~~ Linear

~~Molecular Type:~~ Synthetic DNA

~~Sequence~~

TTACAGGTGA CGGACACTCT GTCACCCAC

29

SEQ ID NO: 50

Sequence Length: 379

~~Sequence Type:~~ Nucleic acid

~~Strandedness:~~ Double

~~Topology:~~ Linear

~~Molecular Type:~~ Synthetic

Original Source

Organism: Mouse and human

Immediate Source

Clone: HEF-RVL-M21e-gk

Amino acid -19--1:leader

Amino acid 1 - 23:FR1

Amino acid 24 - 34:CDR1

Amino acid 35 - 49:FR2

Amino acid 50 - 56:CDR2

Amino acid 57 - 88:FR3

Amino acid 89 - 97:CDR3

Amino acid 98 - 107:FR4

Sequence

ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTC GCA ACA GCT ACA GGT Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly -19 -15 -10 -3	48
GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC Val His Ser Asp Ile Gin Met Thr Gln Ser Pro Ser Ser Leu Ser Ala -1 5 10	96
AGC GTG GGT GAC AGA GTG TCC GTC ACC TGT AAG GCC AGT CAG AAT GTG Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val 15 20 25	144
GGT ACT AAT GTA GCC TCG TAC CAG CAG AAG CCA CGA AAG CCT CCA AAG Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys 30 35 40	192
CTG CTG ATC TAC TCG GCA TCC TAT CCG TAC AGT GGT GTG CCA AGC AGA Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg 45 50 55 60	240
TTC AGC GGT AGC GGT AGC GGT ACC GAC TTC ACC TTC ACC ATC AGC AGC Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser 65 70 75	288
CTC CAG CCA GAG GAC ATC GCC ACC TAC TAC TGC CAG CAA TAT AAC AGC Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser 80 85 90	336
TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA C Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys 95 100 105	379

SEQ ID NO: 51

Sequence Length: 379

Sequence Type: Nucleic acid

Strandedness: Double

Topology: Linear

Molecular Type: Synthetic

Original Source

Organism: Mouse and human

Immediate Source

Clone: HEF-RVL-M21f-gx
Amino acid -19--1:leader
Amino acid 1 - 23:FR1
Amino acid 24 - 34:CDR1
Amino acid 35 - 49:FR2
Amino acid 50 - 56:CDR2
Amino acid 57 - 88:FR3
Amino acid 89 - 97:CDR3
Amino acid 98 - 107:FR4

Sequence

ATG GGA TGG AGC TGT ATC ATG CTC TCC TTG GTA GCA ACA GCT ACA GGT 48
Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly
-19 -15 -10 -5

GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC ACC CTG AGC GCC 96
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala
-1 1 5 10

AGC GTG GGT GAC AGA GTG TCC GTC ACC TGT AAG GCC AGT CAG AAT GTG 144
Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val
15 20 25

GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA AAG GCT CCA AAG 192
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
30 35 40

CTG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA 240
Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg
45 50 55 60

TTC AGC GGT AGC GGT AGC GGT ACC GAC TTC ACC TTC ACC ATC AGC AGC 288
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser
65 70 75

CTC CAG CCA GAG GAC ATC GCC ACC TAC TTC TGC CAG CAA TAT AAC AGC 336
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Tyr Asn Ser
80 85 90

TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA C
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
95 100 105

SEQ ID NO: 52
Sequence Length: 26
Sequence Type: Nucleic acid
Strandedness: Single
Topology: Linear
Molecular Type: Synthetic DNA
Sequence
GACTTCACCT TGACCATCAG CAGCCT 26
SEQ ID NO: 53
Sequence Length: 26
Sequence Type: Nucleic acid
Strandedness: Single
Topology: Linear
Molecular Type: Synthetic DNA
Sequence
CTGCTGATGG TCAAGGTGAA GTCGGT 26
SEQ ID NO: 54
Sequence Length: 379
Sequence Type: Nucleic acid
Strandedness: Double
Topology: Linear
Molecular Type: Synthetic
Original Source
Organism: Mouse and human
Immediate Source
Clone: HEF-RVL-M21g-gr
Amino acid -19--1:leader
Amino acid 1 - 23:FR1
Amino acid 24 - 34:CDR1
Amino acid 35 - 49:FR2
Amino acid 50 - 56:CDR2
Amino acid 57 - 88:FR3

Amino acid 89 - 97:CDR3

Amino acid 98 - 107:FR4

Sequence

ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly	48
-19 -15 -10 -5	
 GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala	96
-1 5 10	
 AGC GTG GGT GAC AGA GTG TCC GTC ACC TGT AAG GCC AGT CAG AAT GTG Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val	144
15 20 25	
 GGT ACT AAT GTA CCC TGG TAC CAG CAG AAG CCA GGA AAG GCT CCA AAG Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys	192
30 35 40	
 CTG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg	240
45 50 55 60	
 TTC AGC GGT AGC GGT ACC GAC TTC ACC TTG ACC ATC AGC AGC Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser	288
65 70 75	
 CTC CAG CCA GAG GAC ATC GCC ACC TAC TTC TGC CAG CAA TAT AAC AGC Leu Gln Pro Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Tyr Asn Ser	336
80 85 90	
 TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA C Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys	379
95 100 105	

SEQ ID NO: 55

Sequence Length: 379

Sequence Type: Nucleic acid

Strandedness: Double

Topology: Linear

Molecular Type: Synthetic

Original Source

Organism: Mouse and human

Immediate Source

Clon : HEF-RVL-M21h-gx

Amino acid -19--1:leader

Amino acid 1 - 23:FR1

Amino acid 24 - 34:CDR1

Amino acid 35 - 49:FR2

Amino acid 50 - 56:CDR2

Amino acid 57 - 88:FR3

Amino acid 89 - 97:CDR3

Amino acid 98 - 107:FR4

Sequence

ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT	48
Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly	
-19 -15 -10 -5	
GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC	96
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala	
-1 1 5 10	
AGC GTG GGT GAC AGA GTG ACC ATC ACC TGT AAG GCC AGT CAG AAT GTG	144
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val	
15 20 25	
GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA AAG GCT CCA AAG	192
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys	
30 35 40	
CTG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA	240
Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg	
45 50 55 60	
TTC AGC GGT AGC GGT AGC GGT ACC GAC TTC ACC TTG ACC ATC AGC AGC	288
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser	
65 70 75	

CTC CAG CCA GAG GAC ATC GCC ACC TAC TAC TGC CAG CAA TAT AAC AGC 336
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser
80 85 90

TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA C 379
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
95 100 105

SEQ ID NO: 56

Sequence Length: 29

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

GGACAGAGTC CAAAGCCGCT GATCTACTC 29

SEQ ID NO: 57

Sequence Length: 29

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

ATCAGCGGCT TTGGACTCTG TCCTGGCTT 29

SEQ ID NO: 58

Sequence Length: 379

Sequence Type: Nucleic acid

Strandedness: Double

Topology: Linear

Molecular Type: Synthetic

Original Source

Organism: Mouse and human

Immediate Source

Clone: HEF-RVL-M2li-gx

Amino acid -19--1:leader

Amino acid 1 - 23:FR1

Amino acid 24 - 34:CDR1

Amino acid 35 - 49:FR2
Amino acid 50 - 56:CDR2
Amino acid 57 - 88:FR3
Amino acid 89 - 97:CDR3
Amino acid 98 - 107:FR4

Sequence

ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT 48
Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly
-19 -15 -10 -5

GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC 96
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala
-1 1 5 10

AGC GTG GGT GAC AGA GTG TCC GTC ACC TGT AAG GCC AGT CAG AAT GTG 144
Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val
15 20 25

GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA CGA CAG ACT CCA AAG 192
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys
30 35 40

CCG CTG ATC TAC TCG GCA TCC TAT CGG TAC ACT GGT GTG CCA AGC AGA 240
Pro Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg
45 50 55 60

TTC AGC GGT AGC CGT AGC GGT ACC GAC TTC ACC TTG ACC ATC AGC AGC 288
Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser
65 70 75

CTC CAG CCA GAG GAC ATC GCC ACC TAC TTC TGC CAG CAA TAT AAC AGC 336
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Tyr Asn Ser
80 85 90

TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA C 379
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
95 100 105

SEQ ID NO: 59

Sequence Length: 26

Sequence Type: Nucleic acid

Strand dness: Singl

Topology: Lin ar

Molecular Type: Synthetic DNA

Sequence

GAGGACATCG CTGACTACTT CTGCCA

26

SEQ ID NO: 60

Sequence Length: 26

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

AAGTAGTCAG CGATGTCCCTC TGGCTG

26

SEQ ID NO: 61

Sequence Length: 379

Sequence Type: Nucleic acid

Strandedness: Double

Topology: Linear

Molecular Type: Synthetic

Original Source

Organism: Mouse and human

Immediate Source

Clone: HEF-RVL-M21j-gk

Amino acid -19--1:leader

Amino acid 1 - 23:FR1

Amino acid 24 - 34:CDR1

Amino acid 35 - 49:FR2

Amino acid 50 - 56:CDR2

Amino acid 57 - 88:FR3

Amino acid 89 - 97:CDR3

Amino acid 98 - 107:FR4

Sequence

ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT

48

Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly

-19

-15

-10

-5

GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC 96
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala
-1 1 5 10

AGC GTG GGT GAC AGA GTG TCC GTC ACC TGT AAG GCC AGT CAG AAT GTG 144
Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val
15 20 25

GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA CAG AGT CCA AAG 192
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys
30 35 40

CCG CTG ATC TAC TCG GCA TCC TAT CCG TAC ACT GGT GTG CCA AGC AGA 240
Pro Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg
45 50 55 60

TTC AGC GGT AGC GGT ACC GAC TTC ACC TTG ACC ATC AGC AGC 288
Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser
65 70 75

CTC CAG CCA GAG GAC ATC GCC GAC TAC TTC TGC CAG CAA TAT AAC AGC 336
Leu Gln Pro Glu Asp Ile Ala Asp Tyr Phe Cys Gln Gln Tyr Asn Ser
80 85 90

TAT CCT CGG GCG TTC GGC CAA GGG ACC AAC GTG GAA ATC AAA C 379
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
95 100 105

SEQ ID NO: 62
Sequence Length: 379
Sequence Type: Nucleic acid
Strandedness: Double
Topology: Linear
Molecular Type: Synthetic
Original Source
Organism: Mouse and human
Immediate Source
Clone: HEF-RVL-M21k-g κ
Amino acid -19--1:leader
Amino acid 1 - 23:FR1

Amino acid 24 - 34:CDR1
Amino acid 35 - 49:FR2
Amino acid 50 - 56:CDR2
Amino acid 57 - 88:FR3
Amino acid 89 - 97:CDR3
Amino acid 98 - 107:FR4

Sequence

ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT 48
Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly
-19 -15 -10 -5

GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC 96
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala
-1 1 5 10

AGC GTG GGT GAC AGA GTG TCC GTC ACC TGT AAG GCC AGT CAG AAT GTG 144
Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val
15 20 25

GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA AAG GCT CCA AAG 192
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
30 35 40

CTG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA 240
Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg
45 50 55 60

TTC AGC GGT AGC GGT ACC GGT ACC GAC TTC ACC TTG ACC ATC ACC AGC 288
Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser
65 70 75

CTC CAG CCA GAG GAC ATC GCC GAC TAC TTC TGC CAG CAA TAT AAC AGC 336
Leu Gln Pro Glu Asp Ile Ala Asp Tyr Phe Cys Gln Gln Tyr Asn Ser
80 85 90

TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA C 379
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
95 100 105

SEQ ID NO: 63

Sequence Length: 379

Sequence Type: Nucleic acid

Strandedness: Doubt

Topology: Linear

Molecular Type: Synthetic

Original Source

Organism: Mouse and human

Immediate Source

Clone: HEF-RVL-M211-gk

Amino acid -19--1: leader

Amino acid 1 - 23:FR1

Amino acid 24 - 34:CDR

Amino acid 35 - 49:FR2

Amino acid 50 - 56:CDR

Amino acid 57 - 88:FR3

Amino acid 89 - 97:CDR3

Summary

ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT
Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly
-18 -15 -10 -5

66

GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala
-1 1 5 10

96

AGC GTG GGT GAC AGA GTG TCC GTC ACC TGT AAG GCC AGT CAG AAT GTG
 Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val
 15 20 25

144

GGT ACT AAT GTA CCC TGG TAC CAG CAG AAG CCA GGA CAG AGT CCA AAG
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys
30 35 40

192

CCG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA
 Pro Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg
 45 50 55 60

TTC AGC GGT AGC GGT ACC GAC TTC ACC ATC AGC AGC 288
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser
65 70 75

CTC CAG CCA GAG GAC ATC GCC ACC TAC TAC TGC CAG CAA TAT AAC AGC 336
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser
80 85 90

TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA C 379
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
95 100 105

SEQ ID NO: 64

Sequence Length: 26

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

CAGAGCCAAA AGTTCCCTGAG CGCCAG 26

SEQ ID NO: 65

Sequence Length: 26

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

CTCAGGAACT TTTGGCTCTG GGTCA 26

SEQ ID NO: 66

Sequence Length: 379

Sequence Type: Nucleic acid

Strandedness: Double

Topology: Linear

Molecular Type: Synthetic

Original Source

Organism: Mouse and human

Immediate Source

Clone: HEF-RVL-M21m-gk
Amino acid -19--1:lead r
Amino cid 1 - 23:FR1
Amino acid 24 - 34:CDR1
Amino acid 35 - 49:FR2
Amino acid 50 - 56:CDR2
Amino acid 57 - 88:FR3
Amino acid 89 - 97:CDR3
Amino acid 98 - 107:FR4

Sequence

ATG	GCA	TGG	AGC	TGT	ATC	ATC	CTC	TCC	TTG	GTA	GCA	ACA	GCT	ACA	GGT	48
Met	Gly	Trp	Ser	Cys	Ile	Ile	Leu	Ser	Leu	Val	Ala	Thr	Ala	Thr	Gly	
-19		-15						-10							-5	
GTC	CAC	TCC	GAC	ATC	CAG	ATC	ACC	CAG	AGC	CAA	AAG	TTC	CTG	AGC	GCC	96
Val	His	Ser	Asp	Ile	Gln	Met	Thr	Gln	Ser	Gln	Lys	Phe	Leu	Ser	Ala	
-1	1				5						10					
AGC	GTG	GGT	GAC	AGA	GTG	ACC	ATC	ACC	TGT	AAG	GCC	AGT	CAG	AAT	GTG	144
Ser	Val	Gly	Asp	Arg	Val	Thr	Ile	Thr	Cys	Lys	Ala	Ser	Gln	Asn	Val	
15			20						25							
GGT	ACT	AAT	GTA	GCC	TGG	TAC	CAG	CAG	AAG	CCA	GGA	CAG	AGT	CCA	AAG	192
Gly	Thr	Asn	Val	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Lys	
30				35					40							
CCG	CTG	ATC	TAC	TCG	GCA	TCC	TAT	CGG	TAC	AGT	GGT	GTG	CCA	AGC	AGA	240
Pro	Leu	Ile	Tyr	Ser	Ala	Ser	Tyr	Arg	Tyr	Ser	Gly	Val	Pro	Ser	Arg	
45				50					55				60			
TTC	AGC	GGT	AGC	GGT	AGC	GGT	ACC	GAC	TTC	ACC	TTC	ACC	ATC	AGC	AGC	288
Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Phe	Thr	Ile	Ser	Ser	
65					70					75						
CTC	CAG	CCA	GAG	GAC	ATC	GCC	ACC	TAC	TAC	TGC	CAG	CAA	TAT	AAC	AGC	336
Leu	Gln	Pro	Glu	Asp	Ile	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Tyr	Asn	Ser	
80					85					90						

TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA C
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
95 100 105

379

SEQ ID NO: 67

Sequence Length: 29

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

GGACAGAGTC CAAAGCTGCT GATCTACTC

29

SEQ ID NO: 68

Sequence Length: 29

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

ATCAGCAGCTT TGGACTCTG TCCTGGCTT

29

SEQ ID NO: 69

Sequence Length: 379

Sequence Type: Nucleic acid

Strandedness: Double

Topology: Linear

Molecular Type: Synthetic

Original Source

Organism: Mouse and human

Immediate Source

Clone: HEF-RVL-M21n-gk

Amino acid -19--1:leader

Amino acid 1 - 23:FR1

Amino acid 24 - 34:CDR1

Amino acid 35 - 49:FR2

Amino acid 50 - 56:CDR2

Amino acid 57 - 88:FR3

Amino acid 89 - 97:CDR3

Amino acid 98 - 107:FR4

Sequence

ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCA GCT ACA GGT	48
Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly	
-19 -15 -10 -5	
GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC	96
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala	
-1 1 5 10	
AGC GTG GGT GAC AGA GTG ACC ATC ACC TGT AAG GCC AGT CAG AAT GTG	144
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val	
15 20 25	
GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GCA CAG AGT CCA AAG	192
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys	
30 35 40	
CTG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA	240
Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg	
45 50 55 60	
TTC AGC GGT AGC GGT AGC ACC GAC TTC ACC TTC ACC ATC AGC AGC	288
Phe Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser	
65 70 75	
CTC CAG CCA GAG GAC ATC GCC ACC TAC TAC TGC CAG CAA TAT AAC AGC	336
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser	
80 85 90	
TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA C	379
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys	
95 100 105	

SEQ ID NO: 70

Sequence Length: 379

Sequence Type: Nucleic acid

Strandedness: Double

Topology: Linear

Molecular Type: Synthetic

Original Source

Organism: Mouse and human

Immediate Source

Clone: HEF-RVL-M21o-gx

Amino acid -19--1:leader

Amino acid 1 - 23:FR1

Amino acid 24 - 34:CDR1

Amino acid 35 - 49:FR2

Amino acid 50 - 56:CDR2

Amino acid 57 - 88:FR3

Amino acid 89 - 97:CDR3

Amino acid 98 - 107:FR4

Sequence

ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT	48
Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly	
-19 -15 -10 -5	
GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA ACC AGC CTG AGC GCC	96
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala	
-1 1 5 10	
AGC GTG GGT GAC AGA GTG ACC ATC ACC TGT AAG GCC AGT CAG AAT GTG	144
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val	
15 20 25	
GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA CAG AGT CCA AAG	192
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys	
30 35 40	
CCG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA	240
Pro Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg	
45 50 55 60	
TTC AGC GGT AGC GGT AGC GGT ACC GAC TTC ACC TTC ACC ATC AGC AGC	288
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser	
65 70 75	

CTC CAG CCA GAG GAC ATC GCC ACC TAC TAC TGC CAG CAA TAT AAC AGC 336
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser
80 85 90

TAT CCT CGG GCG TTC GGC CAA CGG ACC AAG GTG GAA ATC AAA C 379
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
95 100 105

SEQ ID NO: 71

Sequence Length: 23

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

GCTCCAAAGC CGCTGATCTA CTC 23

SEQ ID NO: 72

Sequence Length: 23

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

TAGATCAGCG GCTTTGGAGC CTT 23

SEQ ID NO: 73

Sequence Length: 379

Sequence Type: Nucleic acid

Strandedness: Double

Topology: Linear

Molecular Type: Synthetic

Original Source

Organism: Mouse and human

Immediate Source

Clone: HEF-RVL-M21p-gx

Amino acid 19--1:leader

Amino acid 1 - 23:FR1

Amino acid 24 - 34:CDR1

Amino acid 35 - 49:FR2
Amino acid 50 - 56:CDR2
Amino acid 57 - 88:FR3
Amino acid 89 - 97:CDR3
Amino acid 98 - 107:FR4

Sequence

ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT	48
Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly	
-19 -15 -10 -5	
GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC	96
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala	
-1 1 5 10	
AGC GTG GGT GAC ACA GTG ACC ATC ACC TGT AAG GCC AGT CAG AAT CTG	144
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val	
15 20 25	
GGT ACT AAT GTA GCC TCG TAC CAG CAG AAG CCA GGA AAG GCT CCA AAG	192
Gly. Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys	
30 35 40	
CCG CTG ATC TAC TCG GCA TCC TAT CCG TAC AGT GGT GTG CCA AGC AGA	240
Pro Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg	
45 50 55 60	
TTC AGC GGT AGC GGT AGC GGT ACC GAC TTC ACC TTC ACC ATC AGC AGC	288
Phe Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser	
65 70 75	
CTC CAG CCA GAG GAC ATC GCC ACC TAC TAC TGC CAG CAA TAT AAC AGC	336
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser	
80 85 90	
TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA C	379
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys	
95 100 105	

SEQ ID NO: 74

Sequence Length: 137

Sequence Type: Nucleic acid

Strandedness: Singl

Topology: Linear

Molecular Type: Synth tic DNA

S qu nc

AAGAAGCCTG GGTCCCTAGT GAAGGTCTCC TGCAAGGCTT CTGGCTTCAA CATTAAAGAC 60
ACCTATATAC ACTGGCTGCG CCAGGCTCCA GGACAGGGCC TGGAGTGGAT GGGAAAGGATT 120
GATCCTGAGG ATGGTAA 137

SEQ ID NO: 75

Sequence Length: 111

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

TGAGATCTGA GGACACAGCC TTTTATTCT GTGCAAGTGC CTACTATGTT AACCAAGGACT 60
ACTGGGGCCA AGGGACCACT GTCACCGTCT CCTCAGGTGA GTGGATCCGA C 111

SEQ ID NO: 76

Sequence Length: 130

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

ACCTTCAGTG AGGACCCAGG CTTCTTCACC TCAGGCTCCAG ACTGCACCAAG CTGCACCTGG 60
GAGTGAGCAC CTGGAGCTAC AGCCAGCAAG AAGAAGACCC TCGAGGTCCA GTCCATGGTC 120
GAAGCTTATC 130

SEQ ID NO: 77

Sequence Length: 132

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

AAAGGCTGTG TCCTCAGATC TCAGGCTGCT GAGCTCCATG TAGGCTGTGT TCGTGGATTG 60
GTCTGCAGTG ATTGTGACTC GCCCCCTGGAA CTTCCGGTCA TATTTAGTAT TACCATCCGC 120
AGGATCAATC CT 132

SEQ ID NO: 78
Sequence Length: 25
Sequence Type: Nucleic acid
Strandedness: Single
Topology: Linear
Molecular Type: Synthetic DNA
Sequence

GATAAGCTTC CACCATGGAC TGGAC 25

SEQ ID NO: 79
Sequence Length: 25
Sequence Type: Nucleic acid
Strandedness: Single
Topology: Linear
Molecular Type: Synthetic DNA
Sequence

GTCGGATCCA CTCACCTGAG GAGAC 25

SEQ ID NO: 80
Sequence Length: 409
Sequence Type: Nucleic acid
Strandedness: Double
Topology: Linear
Molecular Type: Synthetic
Original Source

Organism: Mouse and human

Immediate Source

Clone: HEF-RVH-M21-gyl
Amino acid 1 - 19:leader
Amino acid 1 - 30:FR1
Amino acid 31 - 35:CDR1
Amino acid 36 - 49:FR2
Amino acid 50 - 66:CDR2
Amino acid 67 - 98:FR3
Amino acid 99 - 106:CDR3
Amino acid 107 - 117:FR4

Sequence

DRAFT Sequence Database

ATG GAC TCG ACC TGG AGG GTC TTC TTG CTG GCT GIA GCT CCA GGT Met Asp Trp Thr Trp Arg Val Phe Phe Leu Leu Ala Val Ala Pro Gly	48
-19 -15 -10 -5	
 GCT CAC TCC CAG GTG CAG CTG GTG CAG TCT GGA GCT GAG GTG AAG AAG Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys	96
-1 1 5 10	
 CCT GGG TCC TCA GTG AAG GTC TCC TGC AAG GCT TCT GGC TTC AAC ATT Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile	144
15 20 25	
 AAA GAC ACC TAT ATA CAC TGG GTG CGC CAG GCT CCA GGA CAG GGC CTG Lys Asp Thr Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu	192
30 35 40	
 CAG TGG ATG GGA AGG ATT GAT CCT GCG GAT GGT AAT ACT AAA TAT GAC Glu Trp Met Gly Arg Ile Asp Pro Ala Asp Gly Asn Thr Lys Tyr Asp	240
45 50 55 60	
 CCG AAG TTC CAG GGC CGA GTC ACA ATC ACT GCA GAC GAA TCC ACG AAC Pro Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Asn	288
65 70 75	
 ACA GCC TAC ATG GAG CTC AGC AGC CTG AGA TCT GAG GAC ACA GCC TTT Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Phe	336
80 85 90	
 TAT TTC TGT GCA AGT GCC TAC TAT GTT AAC CAG GAC TAC TGG GGC CAA Tyr Phe Cys Ala Ser Ala Tyr Tyr Val Asn Gln Asp Tyr Trp Gly Gln	384
95 100 105	
 GGG ACC ACT GTC ACC GTC TCC TCA G Gly Thr Thr Val Thr Val Ser Ser	409
110 115	
 SEQ ID NO: 81	
Sequence Length: 84	
Sequence Type: Nucleic acid	
Strandedness: Single	
Topology: Linear	

Molecular Type: Synthetic DNA

Sequence

AGCTTGTAC CGTCTCCTCA GGTGGTGGTG GTTCGGGTGG TCGTGGTTCG GGTGGTGGCG 60
GATCGGACAT CCAGATGACC CAGG 84

SEQ ID NO: 82

Sequence Length: 84

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

AATTCCCTGGG CCATCTGGAT GTCCGATCCG CCACCAACCG AACCAACCAC ACCCGAACCA 60
CCACCAACCTG AGGAGACGGT CACA 84

SEQ ID NO: 83

Sequence Length: 34

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

CAGCCATGGC GCAGTGTGCA GCTGGTGCAG TCTG 34

SEQ ID NO: 84

Sequence Length: 41

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

CCACCCGAAC CACCAACCAC TGAGGGAGACG GTGACAGTGG T 41

SEQ ID NO: 85

Sequence Length: 41

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

GGGACCACCTG TCACCGTCTC CTCAGGTGGT GGTGGTTCGG G

41

SEQ ID NO: 86

Sequence Length: 41

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

GGGCTCTGGG TCATCTGGAT GTCCGATCCG CCACCACCCG A

41

SEQ ID NO: 87

Sequence Length: 44

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

TGGGACATCC AGATGACCCA GAGCCCAAGC AGCCTGAGCG CCAG

44

SEQ ID NO: 88

Sequence Length: 57

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

CAAGAATTCT TATTATTTAT CGTCATCGTC TTTGTAGTCT TTGATTTCGA CCTTGTT

57

SEQ ID NO: 89

Sequence Length: 822

Sequence Type: Nucleic acid

Strandedness: Double

Topology: Linear

Molecular Type: Synthetic

Original Source

Organism: Mouse and human

Immediate Source

Clone: pSCFVT7-hM21

Amino acid 1 - 22:leader

Amino acid 23 - 139:H chain V region

Amino acid 140 - 154:Linker

Amino acid 155 - 261:L chain V region

Amino acid 262 - 269:FLAG

Amino acid sequence of Fv polypeptide scFv-hM21 and
nucleotide sequence coding therefor

Sequence

ATG AAA TAC CTA TTG CCT ACG GCA GCC GCT GGA TTG TTA TTA CTC GCT	48
Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala	
5 10 15	
GCC CAA CCA GCC ATG GCG CAG GTG CAG CTG GTG CAG TCT GGA GCT GAG	96
Ala Gln Pro Ala Met Ala Gln Val Gln Leu Val Gln Ser Gly Ala Glu	
20 25 30	
GTG AAG AAG CCT GGG TCC TCA GTG AAG GTC TCC TGC AAG GCT TCT GGC	144
Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly	
35 40 45	
TTC AAC ATT AAA GAC ACC TAT ATA CAC TGG GTG CGC CAG GCT CCA GGA	192
Phe Asn Ile Lys Asp Thr Tyr Ile His Trp Val Arg Gln Ala Pro Gly	
50 55 60	
CAG GGC CTG GAG TGG ATG GCA AGG ATT GAT CCT GCG GAT GGT AAT ACT	240
Gln Gly Leu Glu Trp Met Gly Arg Ile Asp Pro Ala Asp Gly Asn Thr	
65 70 75 80	
AAA TAT GAC CCG AAG TTC CAG GGC CGA GTC ACA ATC ACT GCA GAC GAA	288
Lys Tyr Asp Pro Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Glu	
85 90 95	
TCC ACG AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGA TCT GAG GAC	336
Ser Thr Asn Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp	
100 105 110	

ACA GCC TTT TAT TTC TGT GCA AGT GCC TAC TAT GTT AAC CAG GAC TAC Thr Ala Phe Tyr Phe Cys Ala Ser Ala Tyr Tyr Val Asn Gln Asp Tyr	115	120	125	384	
TGG GGC CAA GGG ACC ACT GTC ACC GTC TCC TCA GGT GGT GGT GGT TCG Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Ser	130	135	140	432	
GGT GGT GGT TCG GGT GGT GGC GGA TCG GAC ATC CAG ATG ACC CAG Gly Gly Gly Ser Gly Gly Ser Asp Ile Gln Met Thr Gln	145	150	155	160	480
AGC CCA AGC AGC CTG AGC GCC AGC GTG GGT GAC AGA GTG ACC ATC ACC Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr	165	170	175	528	
TGT AAG GCC AGT CAG AAT GTG GGT ACT AAT GTA GCC TGG TAC CAG CAG Cys Lys Ala Ser Gln Asn Val Gly Thr Asn Val Ala Trp Tyr Gln Gln	180	185	190	576	
AAG CCA GGA AAG GCT CCA AAG CCG CTG ATC TAC TCG GCA TCC TAT CGG Lys Pro Gly Lys Ala Pro Lys Pro Leu Ile Tyr Ser Ala Ser Tyr Arg	195	200	205	624	
TAC AGT GGT GTG CCA AGC AGA TTC AGC GGT AGC GGT AGC GGT ACC GAC Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Thr Asp	210	215	220	672	
TTC ACC TTC ACC ATC AGC AGC CTC CAG CCA GAG GAC ATC GCT ACC TAC Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr	225	230	235	240	720
TAC TGC CAG CAA TAT AAC AGC TAT CCT CGG GCG TTC GGC CAA GGG ACC Tyr Cys Gln Gln Tyr Asn Ser Tyr Pro Arg Ala Phe Gly Gln Gly Thr	245	250	255	768	
AAG GTC GAA ATC AAA GAC TAC AAA GAC GAT GAC GAT AAA Lys Val Glu Ile Lys Asp Tyr Lys Asp Asp Asp Lys	260	265		807	
TAATAAGAAT TCTTG				822	

SEQ ID NO: 90

Sequence Length: 45

Sequence Type: Nucleic acid

Strandness: Double

Topology: Linear

Molecular Type: Synthetic

Features: Amino acid sequence of linker region of Fv polypeptide
and nucleotide sequence coding therefor

Sequence

GGT GGT GGT GGT TCG GGT GGT GGT TCG GGT GGT CCC GGA TCG
Gly Gly Gly Gly Ser Gly Gly Ser Gly Ser Gly Gly Gly Ser

5

10

15

45